

TFEEDET" 6645000T

BLASTP ALIGNMENT OF SEQ ID NO: 5 WITH ADIPONECTIN POLYPEPTIDE (SEQ ID NO: 402)

Query: Adiponectin-Like Polypeptide (SEQ ID NO: 5)
Subject: --gil5213856 AF404407_1 (AF404407) adiponectin [Macaca mulatta] (SEQ ID NO: 402)
Length = 243

Score = 158 (60.7 bits), Expect = 1.3e-08, P = 1.3e-08

Identities = 42/136 (30%), Positives = 67/136 (49%)

Query: 670 RVAFSAA-RTSNLAPGTLDPQIVFDLLNLLNGLGETFDLQLGRFNCVPVNGTYVFIHFHMLKLA 728
R AFS T P + PI F + N +D G+F+C + G Y F +H+

Sbjct: 111 RSAFSVGLETYVTVP---NMPIRFTKIFYNQONHYDGTGKFHCNIPGLYFYFAYHITVYM 167

Query: 729 VNVPLYVNLMKNEEVLVSAAYANDGAPDHETASNHAILQLFQGDQIWLRLH----RGAIYG 784
+V V+L K ++ ++ Y + + AS +L L GDQ+WL+++ R +Y

Sbjct: 168 KDVK--VSLFKKDKAMLFYDQYQENNVDDQASGSVLLHLEVGQVWLQVYGEGERNGLIYA 225

Query: 785 SSWKYSTFSGYLLYQD 800

+ STF+G+LLY D

Sbjct: 226 DNDNDSTFTGFLLYHD 241

FIG. 1

BLASTP ALIGNMENT OF SEQ ID NO: 5 WITH HUMAN ADIPONECTIN
AMINO ACID SEQUENCE (SEQ ID NO: 404)

Query: Adiponectin-Like Polypeptide (SEQ ID NO: 5)
Subject: AAY85144 13-MAR-2000 09-MAR-1999 20-JUN-2000 09-MAR-1999 Human
adiponectin amino acid sequence. [Homo sapiens] (SEQ ID NO: 404)
Length = 244

Score = 156 (60.0 bits), Expect = 4.3e-09, P = 4.3e-09

Identities = 41/136 (30%), Positives = 67/136 (49%)

Query: 670 RVAFSAA-RTSNLAPGTLDDQPIVFDLLLNILGETFDLQLGRFNCVNGTYVFI F H M L K L A 728
R A F S T P + P F + N + D G + F + C + G Y F + H +

Sbjct: 112 RSAFSVGLETYTYTIP---NMPEFTKIFYNQNNHYDGTGKFCNIPGLYYFAYHITVYM 168

Query: 729 VNVPLYVNLMKNEEVLVSAAYANDGAPDHETASNHAILQLFQGDQIWLRLH---RGAIYG 784
+V V+L K ++ ++ Y +++ AS +L L GDQ+WL+++ R +Y

Sbjct: 169 KDVK--VSLFKKDKAMLFYDQYQENNYDQASGSVLLHLEVGDVWLQVYGEGERNGLYA 226

Query: 785 SSWKYSTFSGYLLYQD 800

+ STF+G+LLY D

Sbjct: 227 DNDNDSTFTGFLLYHD 242

FIG. 2

"FEED" SEQUENCE

BLASTP ALIGNMENT OF SEQ ID NO: 15 WITH ADIPONECTIN POLYPEPTIDE (SEQ ID NO: 402)

Query: Adiponectin-Like Polypeptide (SEQ ID NO: 15)
Subject: gi15213856 AF404407_1 (AF404407) adiponectin [Macaca mulatta] (SEQ ID NO: 402)
Length = 243

Score = 147 (56.8 bits), Expect = 2.6e-07, P = 2.6e-07

Identities = 40/136 (29%), Positives = 65/136 (47%)

Query: 580 RVAFSAA-RTSNLAPGTLDPYGVVDLLLNILGETFDLQLGRFNCVPVNGTYVFIFHMLKLA 638
R AFS T P + P + N +D G+F+C + G Y F +H+

Sbjct: 111 RSAFSVGLETYVTP---NMPIRFTKIFYNQNNHYDGGSTGKFCNIPGLYYFAYHITVYM 167

Query: 639 VNVPLYVNLMKNEEVLSAYANDGAPDHETASNHAILQLFQGDQIWLRLH---RGAIYG 694
+V V+L K ++ ++ Y + + AS +L L GDQ+WL+++ R +Y

Sbjct: 168 KDVK--VSLFKKDKAMLFYDQYQENNVDDQASGSVLLHLEVGDQVWLQVYGEGERNGLYA 225

Query: 695 SSWKYSTFGYLLYQD 710
+ STF+G+LLY D

Sbjct: 226 DNDNDSTFTGFLLYHD 241

FIG. 3

BLASTP ALIGNMENT OF SEQ ID NO: 15 WITH HUMAN ADIPONECTIN
AMINO ACID SEQUENCE (SEQ ID NO: 404)

Query: Adiponectin-Like Polypeptide (SEQ ID NO: 15)
Subject: AAY85144 13-MAR-2000 09-MAR-1999 20-JUN-2000 09-MAR-1999 Human
adiponectin amino acid sequence. [Homo sapiens] (SEQ ID NO: 404)
Length = 244

Score = 151 (58.2 bits), Expect = 1.5e-08, P = 1.5e-08

Identities = 40/136 (29%), Positives = 66/136 (48%)

Query: 580 RVAFSAA-RTSNLAPGTLDPQYGVDDLNNLGETFDLQLGRFNCVPNGTYVFIFHMLKLA 638
R AFS T P + P + N +D G+F+C + G Y F +H+

Sbjct: 112 RSAFSVGLETYTYTIP---NMPERFTKIFYNQNNHYDGTGKFCNIPGLYYFAYHITVYM 168

Query: 639 VNVPLYVNLMKNEEVLVSAAYANDGAPDHETASNHAILQLFQGDQIWLRLH---RGAIYG 694
+V V+L K ++ ++ Y +++ AS +L L GDQ+WL+++ R +Y

Sbjct: 169 KDVK--VSLFKDKKAMLFTYDQYQENNYDQASGSVLLHLEVGQVWLQVYGEGERNGLYA 226

Query: 695 SSWKYSTFSGYLLYQD 710
+ STF+G+LLY D

Sbjct: 227 DNDNDSTFTGFLLYHD 242

FIG. 4

BLASTP ALIGNMENT OF SEQ ID NO: 28 WITH ADIPONECTIN POLYPEPTIDE (SEQ ID NO: 402)

Query: Adiponectin-Like Polypeptide (SEQ ID NO: 28)
 Subject: gi15213856 AF404407_1 (AF404407) adiponectin [Macaca mulatta] (SEQ ID NO: 402)
 length = 243

Score = 351 (128.6 bits), Expect = 7.7e-31, P = 7.7e-31

Identities = 84/225 (37%), Positives = 124/225 (55%)

Query:	525	GPPGFP	GIGKPGVAG-LHGPPKPGALGPQGPGLPGPPPGPPGPPAVMPPTPPPPQGE	583
Sbjct:		GP	+ K G + G PG PG G + G G PG G G P ++ P +G	
	23	GPGVLLPLPKGACTGWMAGIPGHPGHNGVPGRDGRDGPGEKGEKGDPLIGP----	KG- 77	
Query:	584	YLPDMG-LGIDGVKPPHAYGAKKGNGGP----	AYEM-PAFTAELTAPFPPVGPVGFNKL	638
Sbjct:		D G G+ G + P + +G+ G P AY AF+ L P++F K+		
	78	---DTGETGVTGAEGPRGFPGIQGRKGEPEGAYVRSVGLETYVTVPNMPIRFTKI	134	
Query:	639	LYNGRQNYNPQTGIFTCEVPGVYFYFAYHVHCKGNVWVALFKNNEPVMYTYDEYKKGFLD	698	
Sbjct:		YN + +Y+ TG F C +PG+YFYFAYH+ +V V+LFK ++ +++TYD+Y++ +D		
	135	FYNQNHYDGSTGKFHCNIPGLYFYFAYHITVYMKDVKVSFLFKDKAMLFYDQYQENNVD	194	
Query:	699	QASGSVLLLRPGDRVFLQMPSE-QAAGLYAGQYVHSSFSGYLLY	742	
Sbjct:		QASGS +L L GD+V+LQ+ E + GLYA S+F+G+LLY		
	195	QASGSVLLHLEVGQVWLQVYGEGERNGLYADNDNDSTFTGFLLY	239	

FIG. 5

**BLASTP ALIGNMENT OF SEQ ID NO: 28 WITH HUMAN ADIPONECTIN
AMINO ACID SEQUENCE (SEQ ID NO: 404)**

Query: Adiponectin-Like Polypeptide (SEQ ID NO: 28)
 Subject: AAY85144 13-MAR-2000 09-MAR-1999 20-JUN-2000 09-MAR-1999 Human
 adiponectin amino acid sequence. [Homo sapiens] (SEQ ID NO: 404)
 Length = 244

Score = 363 (132.8 bits), Expect = 6.7e-33, P = 6.7e-33

Identities = 87/236 (36%), Positives = 129/236 (54%)

Query:	514	IPGPKGEPLPGPPGPGIGKPGVAG-LHGPPGKPGALGPQGPGLPGLPGPPGPPGPPA	572
		+PG E + GP + K G + G PG PG G + G G PG G G P	
Sbjct:	13	LPGHDQETTIQGPVLLPLPKGACTGWMAGIPGHPGHGAPGRDGRDTPGEKGEKGDPG	72
Query:	573	VMPPTPPPQGEYLPDMG-LGIDGVKPPHAYGAKKGNGP---AYEM-PAFTAELTAPFP	627
		++ P +G D+G G+ G + P + +G+ G P AY AF+ L +	
Sbjct:	73	LIGP----KG----DIGETGVPGAEGPRGPPGIQGRKGEPEGAYVYRSAFSVGLETYT	124
Query:	628	PVGAPVKFNKLLYNGRQNYNPQTGIFTCEVPGVYFYFAYHVHCKGNVWVALFKNNEPVMY	687
		P +F K+ YN + +Y+ TG F C +PG+YFYFAYH+ +V V+LFK ++ +++	
Sbjct:	125	IPNMPERFTKIFYNQNHYDGGTGKFCNCNIPGLYFYFAYHITVYMKDVKVSFLFKDKAMLF	184
Query:	688	TYDEYKKGFLDQASGSVLLLRPGDRVFLQMPSE-QAAGLYAGQYVHSSFSGYLLY	742
		TYD+Y++ DQASGS +L L GD+V+LQ+ E + GLYA S+F+G+LLY	
Sbjct:	185	TYDQYQENNYDQASGSVLLHLEVGQVWLQVYGEGERNGLYADNDNDSTFTGFLLY	240

FIG. 6

BLASTP ALIGNMENT OF SEQ ID NO: 186 WITH ADIPONECTIN POLYPEPTIDE (SEQ ID NO: 402)

Query: Adiponectin-Like Polypeptide (SEQ ID NO: 186)
 Subject: gi15213856 AF404407.1 (AF404407) adiponectin [Macaca mulatta] (SEQ ID NO: 402)
 Length = 243

Score = 472 (171.2 bits), Expect = 1.4e-44, P = 1.4e-44

Identities = 104/204 (50%), Positives = 130/204 (63%)

Query: 86 GIKGDQSGSPGKHGPKGLAGPMGEKGLRGETGPQGQKGNKGDVGTGPEGPRGNIGPL 145
 GI G G G PG+ G G G GEKG G GP KG+ G+ G TG EGPRG G

Sbjct: 41 GIPGHPGHNGVPGRDGRDGTGPEKGEKGDPLIGP---KGDGTGVTGAEGPRGFPGIQ 97

Query: 146 GPTGLPGPMGPIGKPG-PKG-EAGPTGPQDMPKIKFDKILYNEFNHYDTAAGKFTCHIAGV 203
 G G PG + + G E T P +MPI+F KI YN+ NHYD + GKF C+I G+

Sbjct: 98 GRKGEPGEGAYVYRSAPSVGLETYVTVP-NMPIRFTKIFYNQNNHYDGTGKFKHCNIPGL 156

Query: 204 YYFTYHITVFSRNVQVSLVKNGVKILHTKDAYMSSE-DQASGGIVLQLKLGDEVWLQVVG 262
 YYF YHITV+ ++V+VSL K +L T D Y + DQASG ++L L++GD+VWLQV G

Sbjct: 157 YYFAYHITVYMKDVKVSLEFKDKAMLFYDQYQENNVVDQASGSVLLHLEVGDVWLQVVG 216

Query: 263 -GERFNGLFADEDDDTTFTGFLLF 285
 GER NGL+AD D+D+TFTGFLL+

Sbjct: 217 EGER-NGLYADNDNDSTFTGFLLY 239

FIG. 9

BLASTP ALIGNMENT OF SEQ ID NO: 186 WITH HUMAN ADIPONECTIN
AMINO ACID SEQUENCE (SEQ ID NO: 404)

Query: Adiponectin-Like Polypeptide (SEQ ID NO: 186)
Subject: AAY85144 13-MAR-2000 09-MAR-1999 20-JUN-2000 09-MAR-1999 Human
adiponectin amino acid sequence. [Homo sapiens] (SEQ ID NO: 404)
Length = 244

Score = 458 (166.3 bits), Expect = 7.6e-44, P = 7.6e-44

Identities = 102/204 (50%), Positives = 129/204 (63%)

Query: 86 GIKGDQSGRSGPKHGPKGLAGPMGEKGLRGETGPGQKGKNGKGDVGPTGPEGPRGNIGPL 145
GI G G G+PG+ G G G GEKG G GP KG+ G+ G G EGPRG G

Sbjct: 42 GIPGHPGHNGAPGRDGRDGTGPEKGEKGDPLIGP---KGDIGETGVPGAEGPRGFPGIQ 98

Query: 146 GPTGLPGPMGPIGKPG-PKG-EAGPTGPDMPKFDKILYNEFNHYDTAAGKFTCHIAGV 203
G G PG + + G E T P +MP +F KI YN+ NYD + GKF C+I G+

Sbjct: 99 GRKGEPGEGAYVYRSAPSVGLETYTIP-NMPERFTKIFYNQNNHYDGTGKFKHCNIPGL 157

Query: 204 YYFTYHITVFSRNVQVSLVKNVVKILHTKDAYMSSE-DQASGGIVLQKLGDVWLQVTG 262
YYF YHITV+ ++V+VSL K +L T D Y + DQASG ++L L++GD+VWLQV G

Sbjct: 158 YYFAYHITVYMKDVKVSFLFKDKAMLFYDQYQENNYDQASGSVLLHLEVGDVWLQVYG 217

Query: 263 -GERFNGLFADEDDDTFTGFLLF 285
GER NGL+AD D+D+TFTGFLL+

Sbjct: 218 EGER-NGLYADNDNDSTFTGFLLY 240

FIG. 10

BLASTP ALIGNMENT OF SEQ ID NO: 215 WITH ADIPONECTIN POLYPEPTIDE (SEQ ID NO: 402)

Query: Adiponectin-Like Polypeptide (SEQ ID NO: 215)
 Subject: gil5213856 AF404407_1 (AF404407) adiponectin [Macaca mulatta] (SEQ ID NO: 402)
 length = 243

Score = 208 (78.3 bits), Expect = 1.4e-16, P = 1.4e-16

Identities = 57/178 (32%), Positives = 86/178 (48%)

Query:	104	GLAGPMGEKGLRGETGPQCQKGNKGDVGP	TGPEGPRGNIGPLGPTGLPGMPGIGKPGPK	163
		G+ G G G+ G G G KG+ G G	GP+G+ G G TG GP G G G K	
Sbjct:	41	GIPGHPGHNGVPGRDGRDGTGPEKGEKGD	PGLIGPKGDTGVTGAEGPRGFPGIQGRK	100
Query:	164	GEAGPTGPQGEPPVR-GIRGWKGD	RGEKGIGETLVLPKSAFTVGLTVLSKFPSSDVPIK	222
		GE G G+ + + + + + + + + G T K F + +		
Sbjct:	101	GEPGEGAYVYRS	AFSVGLETYVTVPNMPIRFTKIFYNQNNHYD-GST--GKFHCNIPGLY	157
Query:	223	FDKIHITVFSRNVQVSLVKN	GVKILHTRDAYVSSE-DQASGSIVLQLKLGDEMWCVIH	279
		+ HITV+ ++V+VSL K +L T D Y + DQASGS++L I++GD++W ++		
Sbjct:	158	YFAYHITVYMKDVKVS	LFKKDKAMLFYDQYQENNVDQASGSVLLHLEVG	QDVWLIQVY 215

FIG. 11

BLASTP ALIGNMENT OF SEQ ID NO: 215 WITH HUMAN ADIPONECTIN
AMINO ACID SEQUENCE (SEQ ID NO: 404)

Query: Adiponectin-Like Polypeptide (SEQ ID NO: 215)
Subject: AAY85144 13-MAR-2000 09-MAR-1999 20-JUN-2000 09-MAR-1999 Human
adiponectin amino acid sequence. [Homo sapiens] (SEQ ID NO: 404)
Length = 244

Score = 213 (80.0 bits), Expect = 7.0e-18, P = 7.0e-18

Identities = 60/182 (32%), Positives = 91/182 (50%)

Query: 104 GLAGPMGEKGLRGETGPGQKGNKGDVGTGPEGPRGNIGPLGPTGLPGPMCPICKPGPK 163
G+ G G G G G G G KG+ G G GP+G+IG TG+PG GP G PG +

Sbjct: 42 GIPGHPGHNGAPGRDGRDGTGPEKGEKGDPLIGPKGDIGE---TGVPGAEGPRGFPPIQ 98

Query: 164 GEAGPTGPQGEPPVR-----GIRGWKGDGRGEKGKIGETLVLPKSAFTVGLTVLSKFPSSD 218
G G G +G R G+ + + + + + G T KF +

Sbjct: 99 GRKGEPG-EGAYVYRSAPSVGLETTYTIPNMPERFTKIFYNQNNHYD-GST--GKFHCNI 154

Query: 219 VPIKFDKIHTVFSRNVQVSLVKNGVKILHTRDAYVSSE-DQASGSIVLQLKLGDEMWCV 277
+ + HITV+ ++V+VSL K +L T D Y + DQASGS++L L++GD++W

Sbjct: 155 PGLYYFAYHITVYMKDVKVSFLFKDKAMLFYDQYQENNYDQASGSVLLHLEVGQDVWLQ 214

Query: 278 IH 279
++

Sbjct: 215 VY 216

FIG. 12

TFDEQET" 5545000T

BLASTP ALIGNMENT OF SEQ ID NO: 241 WITH ADIPONECTIN POLYPEPTIDE (SEQ ID NO: 402)

Query: Adiponectin-Like Polypeptide (SEQ ID NO: 241)
Subject: gil5213856 AF404407_1 (AF404407) adiponectin [Macaca mulatta] (SEQ ID NO: 402)
Length = 243

Score = 476 (172.6 bits), Expect = 5.4e-45, P = 5.4e-45

Identities = 101/202 (50%), Positives = 129/202 (63%)

Query: 131 GPTGPEGPRGNIGPLGPTGLPGPMGPIGKPGKGEAGTGPQGEQVQGIQGWKGDGRGEK 190
G G G G G G G PG G G PG G G TG. G G +G RG+ G +G K
Sbjct: 41 GIPGHPGHNGVPGRDGRDGTGEGKEKGDPLIGPKGDTGETGVTGAEGPRGFPFIQGRK 100

Query: 191 GKIGETLVLPKSAFTVGLTVLSKFPSSDRPIKFDKILYNEFNHYDTAAGKFTCHIAGVYY 250
G+ GE + +SAF+VGL P+ PI+F KI YN+ NHYD + GKF C+I G+YY
Sbjct: 101 GEPGEGAVVYRSASFVGLETYVTVPNM--PIRFTKIFYNQNNHYDGTGKFGHCNIPGLYY 158

Query: 251 FTYHITVFSRNVQVSLVKNQVKILHTKDAYSSE-DQASGGIVLQLKLGDEVWLQVTG-G 308
F YHITV+ ++V+VSL K +L T D Y + DQASG ++L L++GD+VWLQV G G
Sbjct: 159 FAYHITVYMKDVKVSLFKKDKAMLFYDQYQENNVNQASGSVLLHLEVGQVWLQVYGE 218

Query: 309 ERFNGLFADEDDDTTFTGFLLF 330
ER NGL+AD D+D+TFTGFLL+
Sbjct: 219 ER-NGLYADNDNDSTFTGFLLY 239

FIG. 13

BLASTP ALIGNMENT OF SEQ ID NO: 241 WITH HUMAN ADIPONECTIN
AMINO ACID SEQUENCE (SEQ ID NO: 404)

Query: Adiponectin-Like Polypeptide (SEQ ID NO: 241)
Subject: AAY85144 13-MAR-2000 09-MAR-1999 20-JUN-2000 09-MAR-1999 Human
adiponectin amino acid sequence. [Homo sapiens] (SEQ ID NO: 404)
Length = 244

Score = 473 (171.6 bits), Expect = 2.0e-45, P = 2.0e-45

Identities = 100/202 (49%), Positives = 128/202 (63%)

Query:	131	GPTGPEGPRGNIGPLGPTGLPGPMGPIGKPGKGEAGPTGPQGE	PGVQGIRGWKGD	RGEK	190
		G G			
Sbjct:	42	GIPGHPGHN	GAPGRDGRDGT	PGKEKGD	PLIGPKD
Query:	191	GKIGETLVL	PKSAFTVGLTVLSKFPSSDRPIKFDKILYNEFNHYDTAAGKFT	CHIAGVY	250
		G+ GE + +SAF+VGL	P+ P +F KI YN+ NHYD + GKF C+I G+YY		
Sbjct:	102	GEPEGAYVYRS	AFSVGLETTYTYTIPNM--PERFTKIFYNQONHYD	GSTGK	159
Query:	251	FTYHITVFSRNVQVSLVKN	GVKILHTKDAYMSSE-DQASGGIVLQLKLGDEVWLQ	VTG-G	308
		F YHITV+ ++V+VSL K	+L T D Y + DQASG ++L L++GD+VWLQV G G		
Sbjct:	160	FAYHITVYMKDV	KVSLFKDKKAMLF	TYDQYQENNYDQASGVLLHLEVG	219
Query:	309	ERFNGLFADEDD	DTTFTGFLLF		330
		ER NGL+AD D+D+TFTGFL	L+		
Sbjct:	220	ER-NGLYADNDND	STFTGFLLY		240

FIG. 14

BLASTP ALIGNMENT OF SEQ ID NO: 272 WITH
ADIPOSE TISSUE-SPECIFIC PROTEIN ADIPO Q (SEQ ID NO: 403)

Query: Adiponectin-Like Polypeptide (SEQ ID NO: 272)
Subject: gil14289336 AF269230_1 (AF269230) adipose tissue-specific protein adipon Q
[Bos taurus] (SEQ ID NO: 403) Length = 240

Score = 212 (79.7 bits), Expect = 1.0e-34, Sum P(2) = 1.0e-34

Identities = 41/78 (52%), Positives = 56/78 (71%)

Query: 227 HITVFSRNVQVSLVKNQVILHTKDAYMSSE-DQASGGIVLQLKLGDEVWLQVTGGERFN 285
HITV+ ++V+VSL K +L T D Y DQASG ++L L++GD+VWLQV GE N
Sbjct: 158 HITVYMKDVKVSFLFKKDKAVLFTYDQYQEKNVQDQSGSVLLHLEVGQVWLQVYEGENHN 217

Query: 286 GLFADEDDDTTFTGFLLF 303
G++AD +D+TFTGFL+
Sbjct: 218 GYADNVNDSTFTGFLLY 235

FIG. 15a

BLASTP ALIGNMENT OF SEQ ID NO: 272 WITH
ADIPOSE TISSUE-SPECIFIC PROTEIN ADIPO Q (SEQ ID NO: 403)

Query: Adiponectin-Like Polypeptide (SEQ ID NO: 272)
Subject: gi14289336 AF269230_1 (AF269230) adipose tissue-specific protein adipon Q
[Bos taurus] (SEQ ID NO: 403) Length = 240

Score = 183 (69.5 bits), Expect = 1.0e-34, Sum P(2) = 1.0e-34

Identities = 43/100 (43%), Positives = 56/100 (56%)

Query: 6 LLLAIEICTGNINSQD-----TCRQGHPIPCNPGHNGLPGRDGRDGAKGDKGDAGEPG 59
 LLLA+ G N +D C GIPG+PGHNG PGRDGRDG G+KG+ G+ G
Sbjct: 9 LLLALP-SHGEDNMEDPPLPKGACAGWMAGIPGHPGHNGTTPGRDGRDTPGEKGEKGDAG 67

Query: 60 RPSGPKDGTSGEKGERGADGKVEAKGIKGDQGSRGSPGK 99
 G G+ +G+ G GA+G +G G G +G PG+
Sbjct: 68 LLGPKGE---TGDVGMTGAEGP---RGFPPTPRKKEPGE 101

FIG. 15b

BLASTP ALIGNMENT OF SEQ ID NO: 302 WITH ADIPONECTIN POLYPEPTIDE (SEQ ID NO: 402)

Identities = 82/220 (37%), Positives = 116/220 (52%)

Sbjct: 31 PKGACT---GWMAGIPGH-PGHNHVPGRDGRDGTPEKGEKGDPLIGPKDGTGETGVTG 86

Sbjct: 87 AEGPRGFPIQGRKGPEGEAYVY--RSAFSVGLETYVTVPNMPIRFTKIFYNQOONHYDG 144

Sbjct: 145 STGKFHCNIPGLYYFAYHITVYMKD--VKVSLFKDKAMLFITYDQYQENNVDQAGSVL 201

	LHLE	GD+V+++	G	G+	+G	+N+	STF+GF++Y	D
1	1	1	1	1	1	1	1	1
2	1	1	1	1	1	1	1	1
3	1	1	1	1	1	1	1	1
4	1	1	1	1	1	1	1	1
5	1	1	1	1	1	1	1	1
6	1	1	1	1	1	1	1	1
7	1	1	1	1	1	1	1	1
8	1	1	1	1	1	1	1	1
9	1	1	1	1	1	1	1	1
10	1	1	1	1	1	1	1	1
11	1	1	1	1	1	1	1	1
12	1	1	1	1	1	1	1	1
13	1	1	1	1	1	1	1	1
14	1	1	1	1	1	1	1	1
15	1	1	1	1	1	1	1	1
16	1	1	1	1	1	1	1	1
17	1	1	1	1	1	1	1	1
18	1	1	1	1	1	1	1	1
19	1	1	1	1	1	1	1	1
20	1	1	1	1	1	1	1	1
21	1	1	1	1	1	1	1	1
22	1	1	1	1	1	1	1	1
23	1	1	1	1	1	1	1	1
24	1	1	1	1	1	1	1	1
25	1	1	1	1	1	1	1	1
26	1	1	1	1	1	1	1	1
27	1	1	1	1	1	1	1	1
28	1	1	1	1	1	1	1	1
29	1	1	1	1	1	1	1	1
30	1	1	1	1	1	1	1	1
31	1	1	1	1	1	1	1	1
32	1	1	1	1	1	1	1	1
33	1	1	1	1	1	1	1	1
34	1	1	1	1	1	1	1	1
35	1	1	1	1	1	1	1	1
36	1	1	1	1	1	1	1	1
37	1	1	1	1	1	1	1	1
38	1	1	1	1	1	1	1	1
39	1	1	1	1	1	1	1	1
40	1	1	1	1	1	1	1	1
41	1	1	1	1	1	1	1	1
42	1	1	1	1	1	1	1	1
43	1	1	1	1	1	1	1	1
44	1	1	1	1	1	1	1	1
45	1	1	1	1	1	1	1	1
46	1	1	1	1	1	1	1	1
47	1	1	1	1	1	1	1	1
48	1	1	1	1	1	1	1	1
49	1	1	1	1	1	1	1	1
50	1	1	1	1	1	1	1	1
51	1	1	1	1	1	1	1	1
52	1	1	1	1	1	1	1	1
53	1	1	1	1	1	1	1	1
54	1	1	1	1	1	1	1	1
55	1	1	1	1	1	1	1	1
56	1	1	1	1	1	1	1	1
57	1	1	1	1				

Sbjct: 202 LHLEVGQVWLQVYGEGERNGLYADNDNDSTFTGFLLYHD 241

FIG. 17

BLASTP ALIGNMENT OF SEQ ID NO: 302 WITH HUMAN ADIPONECTIN
AMINO ACID SEQUENCE (SEQ ID NO: 404)

Query: Adiponectin-Like Polypeptide (SEQ ID NO: 302)
Subject: AAY85144 AAY85144 13-MAR-2000 09-MAR-1999 20-JUN-2000 09-MAR-1999 Human
adiponectin amino acid sequence. [Homo sapiens] (SEQ ID NO: 404)
Length = 244

Score = 336 (123.3 bits), Expect = 5.8e-31, P = 5.8e-31

Identities = 83/220 (37%), Positives = 117/220 (53%)

Query: 124 PSTAATPDRGLMQSLPTFIQPKGEAGRPKGAGPRGPPGPPGPMGPPGKEGEPGRQG 183
P A T G M +P G G GR G+ G GE G PG +GP G+ GE G G

Sbjct: 32 PKGACT---GWMAGIPGH-PGHNGAPGRDGRDGTPEKEKGDPLIGPKGDIGETGVPG 87

Query: 184 LPGPPGAPGLNAA-GAISAATYSTGPKIAFYAGLKRQHEGYEVL-KFDDVVVTLGNHYDP 241
GP G PG+ G Y + AF GL+ + + +F + N NHYD

Sbjct: 88 AEGPRGFPGIQGRKGEPEGAYVY--RSAFSVGLETYTIPNMPERFTKIFYNQNHYDG 145

Query: 242 TTGKFTCSIPGIYFFTYHVLMRGGDGTSMWADLCKNNQVRASAIADQADQNYDYASNSVV 301
+TGKF C+IPG+Y+YF YH+ + D + L K ++ Q + NYD AS SV+

Sbjct: 146 STGKFHCNIPGLYFYFAYHITVYMKD---VKVSLFKKDKAMLFYDQYQENNYDQASGSVL 202

Query: 302 LHLEPGDEVYIKLDG-GKAHG--GNNNKYSTFSGFIIYAD 338
LHLE GD+V++++ G G+ +G +N+ STF+GF++Y D

Sbjct: 203 LHLEVGDAQVWLQVYGEGERNGLYADNDNDSTFTGFLLYHD 242

FIG. 18

BLASTP ALIGNMENT OF SEQ ID NO: 323 WITH HUMAN ADIPONECTIN
AMINO ACID SEQUENCE (SEQ ID NO: 404)

Query: Adiponectin-Like Polypeptide (SEQ ID NO: 323)
Subject: AAY85144 AAY85144 13-MAR-2000 09-MAR-1999 20-JUN-2000 09-MAR-1999 Human
adiponectin amino acid sequence. [Homo sapiens] (SEQ ID NO: 404)
Length = 244

Score = 336 (123.3 bits), Expect = 5.8e-31, P = 5.8e-31

Identities = 83/220 (37%), Positives = 117/220 (53%)

Query: 30 PSTAATPDRGLMQSLPTFIQPKGEAGRPGKAGPRGPPGPPGPMGPPGKGEPRQG 89
P A T G M +P G G GR G+ G G GE G PG +GP G+ GE G G

Sbjct: 32 PKGACT---GWMAGIPGH-PGHNGAPGRDGRDTPGEKGEKGDPLIGPKGDIGETGVPG 87

Query: 90 LPGPPGAPGLNAA-GAISAATYSTGPKIAFYAGLKRQHEGYEVL-KFDDVVVTLGNHYDP 147
GP G PG+ G Y + AF GL+ + +F + N NHYD

Sbjct: 88 AEGPRGFPGIQGRKGEPEGAYVY--RSAFSVGLETYTYTIPNMPERFTKIFYNQNHYDG 145

Query: 148 TTGKFTCSIPGIYFFTYHVMRGDGTSMWADLCKNNQVRASAIADQADQNYDYASNSV 207
+TGKF C+IPG+Y+F YH+ + D + L K ++ Q + NYD AS SV+

Sbjct: 146 STGKFHCNIPGLYYFAYHITVYMKD---VKVSLFKKDKAMLFYDQYQENNYDQASGSVL 202

Query: 208 LHLEPGDEVYIKLDG-GKAHG--GNNNKYSTFSGFIIYAD 244
LHLE GD+V++++ G G+ +G +N+ STF+GF++Y D

Sbjct: 203 LHLEVGDAQVWLQVYGEGERNGLYADNDNDSTFTGFLLYHD 242

FIG. 20

BLASTP ALIGNMENT OF SEQ ID NO: 348 WITH ADIPONECTIN POLYPEPTIDE (SEQ ID NO: 402)

Query: Adiponectin-Like Polypeptide (SEQ ID NO: 348)
 Subject: gil15213856 AF404407_1 (AF404407) adiponectin [Macaca mulatta] (SEQ ID NO: 402)
 Length = 243

Score = 138 (53.6 bits), Expect = 1.9e-06, P = 1.9e-06

Identities = 69/220 (31%), Positives = 90/220 (40%)

Query:	296	PQPPGSTGVIAETGQAGPPAGAGVSGR-GLPRGVDGQTSGTVPGAEGFAGAPGYPKSPP	354
Sbjct:		P PG GV G+ G P G GL G G TG V GAEG G PG	
Query:	43	PGHPGHNGVPGRDGRDGTGPEKGEKGDPLI-GPKGDTGETGVTGAEGPRGFPGIQGRKG	101
Sbjct:			
Query:	355	VASPGAPVPSLVFSAGL-TQKPPPSDGGVVLFNKVLVNDGDVYNPSTGVFTAPYDGRYL	413
Sbjct:		GA V +FS GL T P+ + F K+ N + Y+ STG F G Y	
Query:	102	EPGEGAYVYRS-AFSVGLETYVTVPNMP--IRFTKIFYNQNHVDGSTGKFCNIPGLYY	158
Sbjct:			
Query:	414	ITATLTPERDAYVEAV-LSVSNASVAQLHTAGYRREFLEYHRPTGALHTCGGPGAFHLIV	472
Sbjct:		+T Y++ V +S+ A L T Y + ++ G +++	
Query:	159	FAYHIT----VYMKDVKVSFLFKDKAMLFT--Y-----DQYQENNVVDQASGS-----VLL	202
Sbjct:			
Query:	473	HLKAGDAVNVVVTG-----GKLAHTDFDEMYSTFSGVFLY	507
Sbjct:		HL+ GD V + V G G A D D STF+G LY	
Query:	203	HLEVGDDQVWLQVYGEGERNGLYADNDND---STFTGFLLY	239
Sbjct:			

FIG. 21

BLASTP ALIGNMENT OF SEQ ID NO: 348 WITH HUMAN ADIPONECTIN
AMINO ACID SEQUENCE (SEQ ID NO: 404)

Query: Adiponectin-Like Polypeptide (SEQ ID NO: 348)
Subject: AAY85144 13-MAR-2000 09-MAR-1999 20-JUN-2000 09-MAR-1999 Human
adiponectin amino acid sequence. [Homo sapiens] (SEQ ID NO: 404)
Length = 244

Score = 132 (51.5 bits), Expect = 1.7e-06, P = 1.7e-06

Identities = 75/243 (30%), Positives = 98/243 (40%)

Query: 269 PRPSGPATAEDPGRRPVLQRPPPEERPPQPPGSTGVIAETGQAGPPAGAGVSGRGLPRGV 328
P P G T G +P P P G G E G+ G P G+ G P+G
Sbjct: 30 PLPKGACTGWMAG----IPGHPGHNGAPGRDGRDGTGPEKEKGDG---GLIG---PKGD 79

Query: 329 DGQTGSGTVPGAEGFAGAPGYPKSPVSPGAPVPSLVSFSAGL-TQKPFPSDGGVVLFN 387
G+TG VPGAEG G PG GA V +FS GL T P+ F
Sbjct: 80 IGETG---VPGAEGPRGPGIQGRKGEPEGAYVYRS-AFSVGLETYTYTIPNMPE--RFT 133

Query: 388 KVLVNDGDEVNPNPSTGVFTAPYDGRYLITATLTPERDAYVEAV-LSVSNASVAQLHTAGYR 446
K+ N + Y+ STG F G Y +T Y++ V +S+ A L T
Sbjct: 134 KIFYNQNHYDGGSTGKFCNIPGLYYFAYHIT----VYMKDVKVSLEFKDKAMLFYDQY 189

Query: 447 REFLEYHRPTGA--LHTCGGPGAFHLIVHLKAGDAVNVVVTGGKLAHTDFDEMYSTFSGV 504
+E Y + +G+ LH G + L V+ G+ G A D D STF+G
Sbjct: 190 QEN-NYDQASGSVLLHLEVGQVW-LQVY---GEGE-----NGLYADNDND---STFTGF 237

Query: 505 FLY 507
LY
Sbjct: 238 LLY 240

FIG. 22

BLASTP ALIGNMENT OF SEQ ID NO: 355 WITH ADIPONECTIN POLYPEPTIDE (SEQ ID NO: 402)

Query: Adiponectin-Like Polypeptide (SEQ ID NO: 355)
 Subject: gil5213856 AF404407_1 (AF404407) adiponectin [Macaca mulatta] (SEQ ID NO: 402)
 Length = 243

Score = 199 (75.1 bits), Expect = 1.2e-15, P = 1.2e-15

Identities = 53/134 (39%), Positives = 68/134 (50%)

Query:	37	PRGPGPDGAPASVPPFP-----PGAKGEVRRGKAGLRGPPGPPGPRGPPGPRPPG	91
		P+G G A +P P PG G G G+ G +G PG GP+G GE G G G	
Sbjct:	31	PKG-ACTGWMAGIPGHPGHNGVPGRDGRDGTGPEKGEKDPGLIGPKGDTGETGVTGAEG	89
Query:	92	PPG-PGPGGVA--PAAG-YVPRIAFYAGLRPPHEGYEV-LRFDDVVTVNNGNAYEAAASGKF	146
		P G PG G P G YV R AF GL + +RF + N N Y+ ++GKF	
Sbjct:	90	PRGFPGIQGRKGEPEGAYVYRSAFSVGLETYVTVPNMPPIRFTKIFYNQQNHVDGSGTGKF	149
Query:	147	TCPMPGVYFFAYHV	160
		C +PG+Y+FYH+	
Sbjct:	150	HCNIPGLYFYFAYHI	163

FIG. 23

BLASTP ALIGNMENT OF SEQ ID NO: 355 WITH HUMAN ADIPONECTIN
AMINO ACID SEQUENCE (SEQ ID NO: 404)

Query: Adiponectin-Like Polypeptide (SEQ ID NO: 355)
Subject: AAY85144 13-MAR-2000 09-MAR-1999 20-JUN-2000 09-MAR-1999 Human
adiponectin amino acid sequence. [Homo sapiens] (SEQ ID NO: 404)
Length = 244

Score = 204 (76.9 bits), Expect = 6.3e-17, P = 6.3e-17

Identities = 54/134 (40%), Positives = 69/134 (51%)

Query: 37 PRGPGPDGAPASVPPFP-----PGAKGEVRRGKAGLRGPPPGPPGPPGPPGPPG 91
P+G G A +P P PG G G G+ G +G PG GP+G GE G PG G

Sbjct: 32 PKG-ACTGWMAGIPGHPGHNGAPGRDGTGPEKGEKDPGLIGPKDIGETGVPGAEG 90

Query: 92 PPG-PGPGGVA--PAAAG-YVPRIAFYAGLRPPHEGYEVL-RFDDVVTNVGNAYEAASGKF 146
P G PG G P G YV R AF GL + + RF + N N Y+ ++GKF

Sbjct: 91 PRGFPGIQGRKGEPGEGAYVYRSFVSGLETTYTIPNMPERFTKIFYNQNHYDGTGKF 150

Query: 147 TCPMPGVYFFAYHV 160
C +PG+Y+FYH+

Sbjct: 151 HCNIPGLYYFAYHI 164

FIG. 24

BLASTP ALIGNMENT OF SEQ ID NO: 378 WITH ADIPONECTIN POLYPEPTIDE (SEQ ID NO: 402)

Query: Adiponectin-Like Polypeptide (SEQ ID NO: 378)
 Subject: gil5213856 AF404407_1 (AF404407) adiponectin [Macaca mulatta] (SEQ ID NO: 402)
 Length = 243

Score = 297 (109.6 bits), Expect = 5.0e-26, P = 5.0e-26

Identities = 80/215 (37%), Positives = 113/215 (52%)

Query:	37	PRGPGPDGAPASVPPFP-----PGAKGEVRRGKAGLRGPPGPPGPPGPPGPPGPPG	91
		P+G G A +P P PG G G G+ G +G PG GP+G GE G G G	
Sbjct:	31	PKG-ACTGWMAGIPGHPGHNGVPGRDGRDTPGEKGEKDPGLIGPKDGTGETGVTGAEG	89
Query:	92	PPG-PGPGGVA--PAAG-YVPRIAFYAGLRRPHEGYEV-LRFDDVVTNVGNAYEAAAGKF	146
		P G PG G P G YV R AF GL + +RF + N N Y+ ++GKF	
Sbjct:	90	PRGFPGIQGRKGEPEGAYVYRSAFSVGLETYVTVPNMPIRFTKIFYNQNNHYDGGSTGKF	149
Query:	147	TCPMPGVYFFAYHVLMRGGDGTSMWADLMKNGQVRSASIAQADQNDYASNSVILHLDV	206
		C +PG+Y+YFAYH+ + D + L K + Q + N D AS SV+LHL+V	
Sbjct:	150	HCNIPGLYFYFAYHITVYMKD---VKVSLFKDKKAMLFYDYQYQENNVDQASGVSILLHLEV	206
Query:	207	GDEVFIKLDG-GKVHG--GNTNKYSTFSGFIIYPD	238
		GD+V++++ G G+ +G + + STF+GF++Y D	
Sbjct:	207	GDQVWLQVYGEGERNGLYADNDNDSTFTGFLLYHD	241

FIG. 25

TOE02T 664500T

BLASTP ALIGNMENT OF SEQ ID NO: 378 WITH HUMAN ADIPONECTIN
AMINO ACID SEQUENCE (SEQ ID NO: 404)

Query: Adiponectin-Like Polypeptide (SEQ ID NO: 378)
Subject: AAY85144 AAY85144 13-MAR-2000 09-MAR-1999 20-JUN-2000 09-MAR-1999 Human
adiponectin amino acid sequence. [Homo sapiens] (SEQ ID NO: 404)
Length = 244

Score = 310 (114.2 bits), Expect = 3.7e-28, P = 3.7e-28

Identities = 82/215 (38%), Positives = 115/215 (53%)

Query: 37 PRGPGPDGAPASVPPFP-----PGAKGEVGRRGKAGLRGPPGPPGPPGPPGPPGPPG 91
P+G G A +P P PG G G G+ G +G PG GP+G GE G PG G
Sbjct: 32 PKG-ACTGWMAGIPGHPGNGAPGRDGTGPGKEKGDPGLIGKGDIGETGVPGAEG 90

Query: 92 PPG-PGPGGVA--PAAG-YVPRIAIFYAGLRRPHEGYEVL-REDDVVTVNGNAYEAASGKF 146
P G PG G P G YV R AF GL + + RF + N N.Y+ ++GKF
Sbjct: 91 PRGFPGIQGRKGEPGEGAYVYSAFVSGLETTYITIPNMPERFKIFYNQNHVDGSGTKGF 150

Query: 147 TCPMPGVYFFAYHVLMRGGDGTSMWADLMKNGQVRASAIQAQADQNYDYASNSVILHLDV 206
C +PG+Y+FYAYH+ + D + L K + Q + NYD AS SV+LHL+V
Sbjct: 151 HCNIPGLYFYAYHITVYMKD---VKVSLFKDKAMLFYDYQYQENNYDQASGSVLLHLEV 207

Query: 207 GDEVFIKLDG-GKVHG--GNTNKYSTFGFIYPD 238
GD+V++++ G G+ +G + + STF+GF++Y D
Sbjct: 208 GDQVWLQVYGEGERNGLYADNDNDSTFTTGLLYHD 242

FIG. 26